Fig. 1

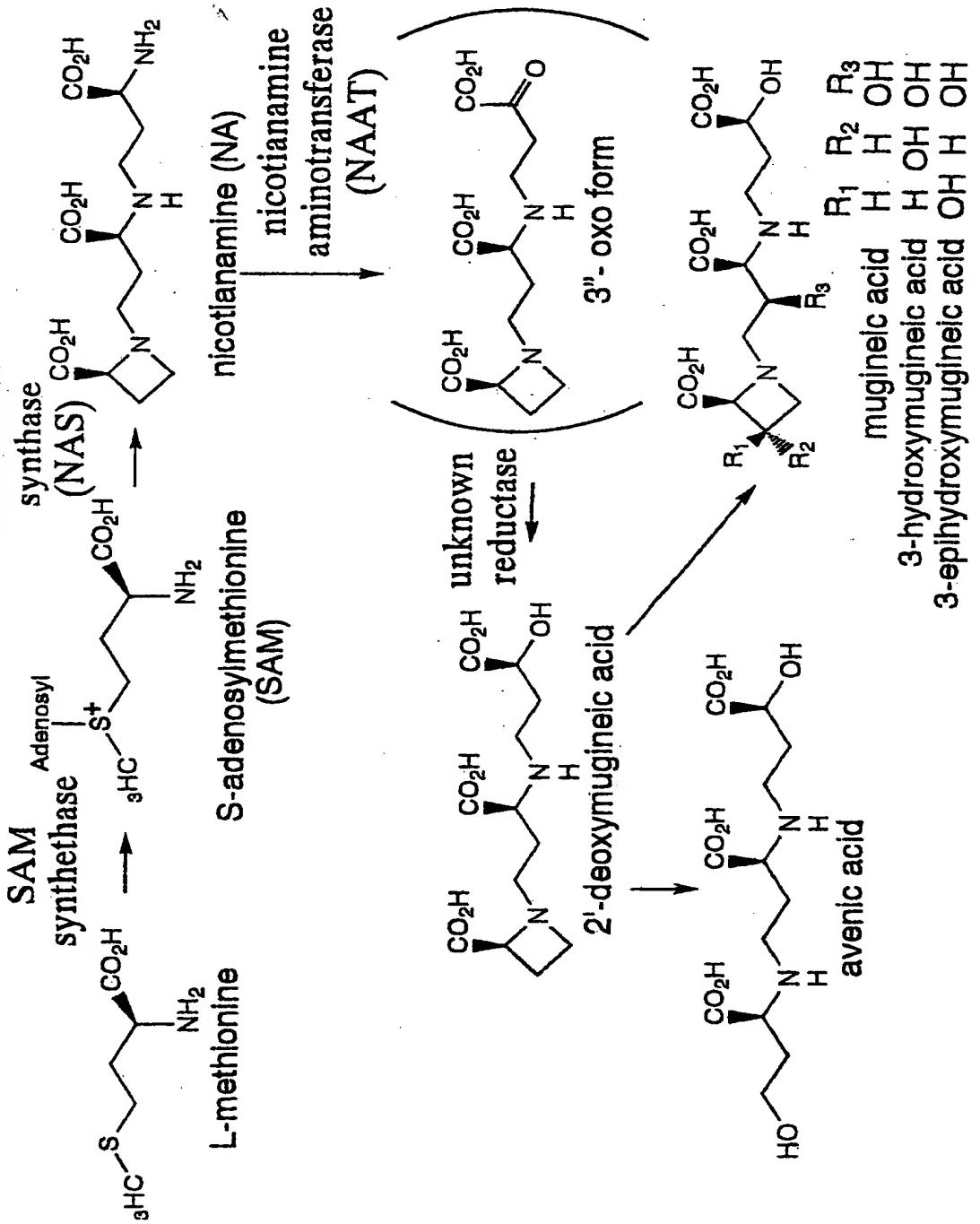


Fig. 2

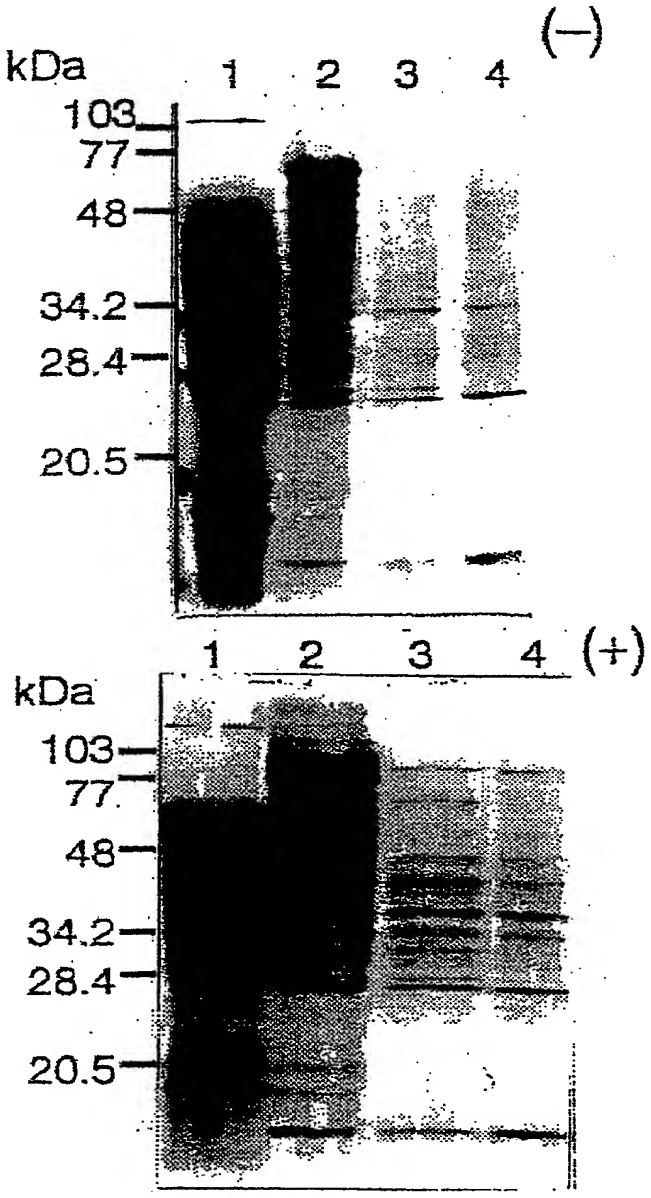


Fig. 3

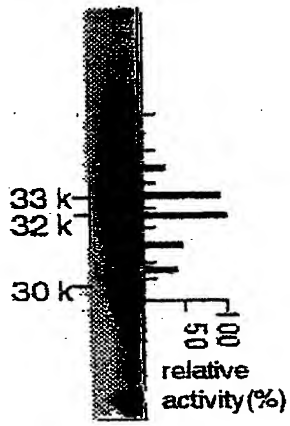


Fig. 4

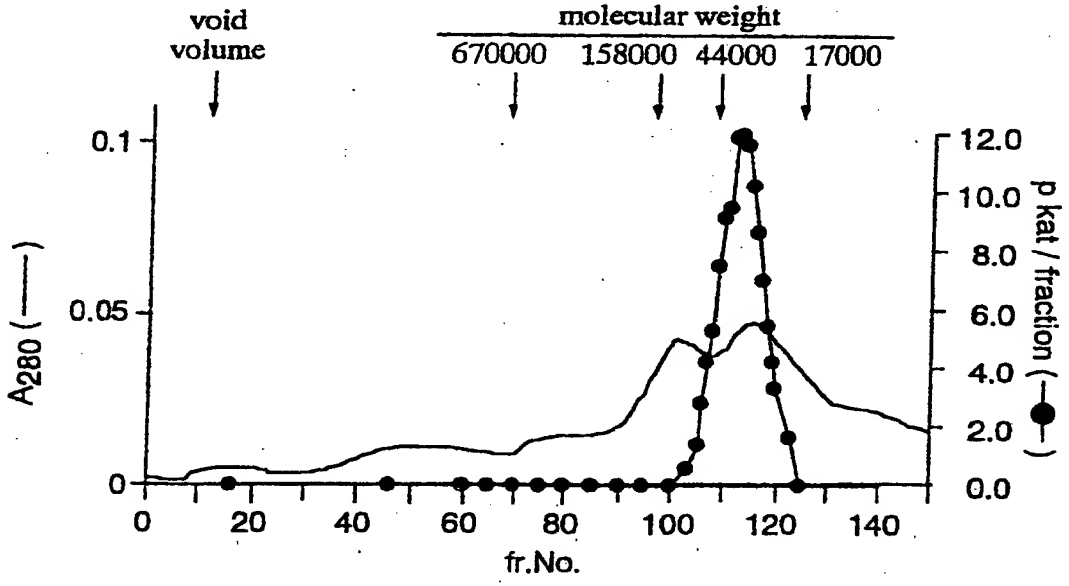


Fig. 5

```
33,32 kDa -1      DAQNKEVAALIEKIAGIQA                                                   33,32 kDa -2  REALIRL
                   ::: ::::: :::::  :                                                                 :: ::::
rice (D24790)     MEAQNQEVAALVEKIAGLHAAISKLPSLSPSAEVDALFTDLVTACVPASPVDVAKLGPEAQAMREELIRLC
                  NF primer →                                                         ← NR primer

rice (D23792)     YVNLSKLEYDLLVRYVPGIAPTRVAFVGSGPLPFSSLVLAAHHLPDAVFDNYDRCGAANERARRLFRGADEGLGARM~
                    IF primer →
                 ~AFHTGDVATLTGELGAYDVVFLATLVGMAAEEKP
                                         ← IR primer
                   ::: ::: :: ::::::::::: :: ::::::
33,32 kDa -3      SFHTADVADLTQELGAYDVVFLAALVDMAAEEKAKVIAHLGAHMVEGASLVVYSAHGARGFLYP
                   :::: : ::: :::::::                       :: ::  :::::: ::::
30 kDa -1         AFHTAEVTDLTAELGAYDV                30 kDa -2  ADGAVLVARSAHGARAFLYPVVELDDVGR

33,32 kDa -4      PEDIRRGGFEVLAVHHPEGE
```

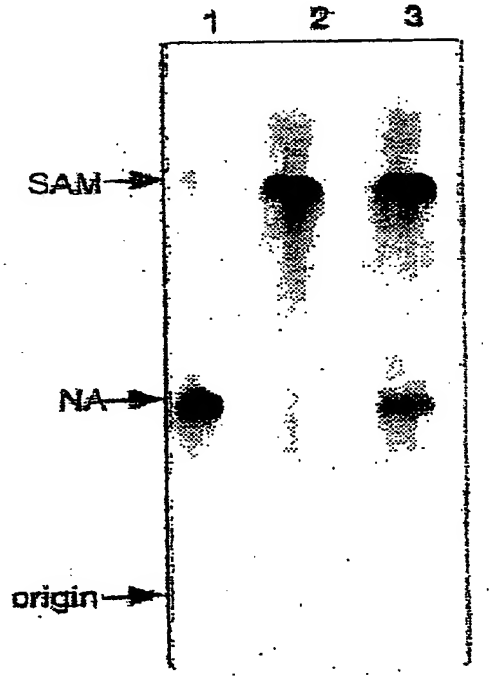
Fig. 6

```
                GCG TTC AGA GGC TTC CAG AGT TCT TCC GGT CAC CAA GAA GCA TTT GAT CAT AAC    54

ATG GAT GCC CAG AAC AAG GAG GTC GCT GCT CTG ATC GAG AAG ATC GCC GGT ATC               108
 19  M  D  A  Q  N  K  E  V  A  A  L  I  E  K  I  A  G  I
     (1)

CAG GCC GCC ATC GCC GAG CTG CCG TCG CTG AGC CCG TCC CCC GAG GTC GAC AGG               162
 37  Q  A  A  I  A  E  L  P  S  L  S  P  S  P  E  V  D  R

CTC TTC ACC GAC CTC GTC ACG GCC TGC GTC CCG CCG AGC CCC GTC GAC GTG ACG               216
 55  L  F  T  D  L  V  T  A  C  V  P  P  S  P  V  D  V  T

AAG CTC AGC CCG GAG CAC CAG AGG ATG CGG GAG GCT CTC ATC CGC TTG TGC TCC               270
 73  K  L  S  P  E  H  Q  R  M  R  E  A  L  I  R  L  C  S
                              (2)

GCC GCC GAG GGG AAG CTC GAG GCG CAC TAC GCC GAC CTG CTC GCC ACC TTC GAC               324
 91  A  A  E  G  K  L  E  A  H  Y  A  D  L  L  A  T  F  D

AAC CCG CTC GAC CAC CTC GGC CTC TTC CCG TAC TAC AGC AAC TAC GTC AAC CTC               378
109  N  P  L  D  H  L  G  L  F  P  Y  Y  S  N  Y  V  N  L

AGC AGG CTG GAG TAC GAG CTC CTG GCG CGC CAC GTG CCG GGC ATC GCG CCG GCG               432
127  S  R  L  E  Y  E  L  L  A  R  H  V  P  G  I  A  P  A

CGC GTC GCC TTC GTC GGC TCC GGC CCG CTG CCG TTC AGC TCG CTC GTC CTC GCC               486
145  R  V  A  F  V  G  S  G  P  L  P  F  S  S  L  V  L  A

GCG CAC CAC CTG CCC GAG ACC CAG TTC GAC AAC TAC GAC CTG TGC GGC GCG GCC               540
163  A  H  H  L  P  E  T  Q  F  D  N  Y  D  L  C  G  A  A

AAC GAG CGC GCC AGG AAG CTG TTC GGC GCG ACG GCG GAC GGC GTC GGC GCG CGT               594
181  N  E  R  A  R  K  L  F  G  A  T  A  D  G  V  G  A  R

ATG TCG TTC CAC ACG GCG GAC GTC GCC GAC CTC ACC CAG GAG CTC GGC GCC TAC               648
199  M  S  F  H  T  A  D  V  A  D  L  T  Q  E  L  G  A  Y
     (3)

GAC GTG GTC TTC CTC GCC GCG CTC GTC GGC ATG GCA GCC GAG GAG AAG GCC AAG               702
217  D  V  V  F  L  A  A  L  V  G  M  A  A  E  E  K  A  K

GTG ATT GCC CAC CTG GGC GCG CAC ATG GTG GAG GGG GCG TCC CTG GTC GTG CGG               756
235  V  I  A  H  L  G  A  H  M  V  E  G  A  S  L  V  V  R

AGC GCA CGG CCC CGC GGC TTT CTT TAC CCC ATT GTC GAC CCG GAG GAC ATC AGG               810
253  S  A  R  P  R  G  F  L  Y  P  I  V  D  P  E  D  I  R
                                          (4)

CGG GGT GGG TTC GAG GTG CTG GCC GTG CAC CAC CCG GAA GGT GAG GTG ATC AAC               864
271  R  G  G  F  E  V  L  A  V  H  H  P  E  G  E  V  I  N

TCT GTC ATC GTC GCC CGT AAG GCC GTC GAA GCG CAG CTC AGT GGG CCG CAG AAC               918
289  S  V  I  V  A  R  K  A  V  E  A  Q  L  S  G  P  Q  N

GGA GAC GCG CAC GCA CGG GGC GCG GTG CCG TTG GTC AGC CCG CCA TGC AAC TTC               972
307  G  D  A  H  A  R  G  A  V  P  L  V  S  P  P  C  N  F

TCC ACC AAG ATG GAG GCG AGC GCG CTT GAG AAG AGC GAG GAG CTG ACC GCC AAA              1026
325  S  T  K  M  E  A  S  A  L  E  K  S  E  E  L  T  A  K

GAG CTG GCC TTT TGA TTG AAG AGT GCG CGT GGT CAT TCT GTC GCC TGC GAT CGT              1080
 E  L  A  F  *

GGT AAC TTT CCT ACT CGT GTG TGT TTT GAT GTT TGT GCC TGT AAG AGT TAT GCT              1134
TCC GGC CTT GTG CTG TTA ATT TAC ACG CGT TAC ATG TAG TAC TTG TAT TTA TAC              1188
CTG GAA TAA CGG TAT GTA ACA TAA ATA TTA GTG GGA TTT GAA GTG TAA TGC TAA              1242
ATA ATA AGA AAA CTT GAT GCA GAC ATT CAA AAA AAA AAA AAA AAA AAA AAA AA
```

Fig. 7

```
HvNAS4   MDGQSE--EVDALVQKITGLHAAIAKLPSLSPSPDVDALFTDLVTACVPPSPVDVTKLAP
HvNAS7   MDAQSK--EVDALVQKITGLHAAIAKLPSLSPSPDVDALFTDLVTACVPPSPVDVTKLAP
HvNAS6   MDAQNK--EVDALVQKITGLHAAIAKLPSLSPSPDVDALFTDLVTACVPPSPVDVTKLGS
HvNAS2   MAAQNN-QEVDALVEKITGLHAAIAKLPSLSPSPDVDALFTELVTACVPPSPVDVTKLGP
HvNAS3   MAAQNNNKDVAALVEKITGLHAAIAKLPSLSPSPDVDALFTELVTACVPPSPVDVTKLGP
HvNAS1   MDAQNK--EVAALIEKIAGIQAAIAELPSLSPSPEVDRLFTDLVTACVPPSPVDVTKLSP
HvNAS5   MEAENG--EVAALVEKITGLHAAISKLPALSPSPQVDALFTELVAACVPSSPVDVTKLGP
         *         * **  ** *  ***  ** ***** ** *** ** **** ********

HvNAS4   EAQAMREGLIRLCSEAEGKLEAHYSDMLAAFDNPLDHLGVFPYYSNYINLSKLEYELLAR
HvNAS7   EAQAMREGLIRLCSEAEGKLEAHYSDMLAAFDNPLDHLGVFPYYSNYINLSKLEYELLAR
HvNAS6   EAQEMREGLIRLCSEAEGKLEAHYSDMLAAFDNPLDHLGMFPYYSNYINLSKLEYELLAR
HvNAS2   EAQEMREGLIRLCSEAEGKLEAHYSDMLAAFDKPLDHLGMFPYYNNYINLSKLEYELLAR
HvNAS3   EAQEMREGLIRLCSEAEGKLEAHYSDMLAAFDNPLDHLGIFPYYSNYINLSKLEYELLAR
HvNAS1   EHQRMREALIRLCSAAEGKLEAHYADLLATFDNPLDHLGLFPYYSNYVNLSRLEYELLAR
HvNAS5   EAQEMRQDLIRLCSAAEGLLEAHYSDMLTALDSPLDHLGRFPYFDNYVNLSKLEHDLLAG
         * * **  ****** *** ***** * *   * ****** ***  ** *** **  ***

HvNAS4   YVPGRHRPARVAFIGSGPLPFSSYVLAARHLPDTVFDNYDLCGAANDRATRLFRADKD-V
HvNAS7   YVPGGIAPARVAFIGSGPLPFSSYVLAARHLPDTVFDNYVPVRAANDRATRLFRADKD-V
HvNAS6   YVPGGIARPAVAFIGSGPLPFSSYVLAARHLPDAMFDNYDLCSAANDRASKLFRADKD-V
HvNAS2   YVPGGYRPARVAFIGSGPLPFSSFVLAARHLPDTMFDNYDLCGAANDRASKLFRADRD-V
HvNAS3   YVRR-HRPARVAFIGSGPLPFSSFVLAARHLPDTMFDNYDLCGAANDRASKLFRADTD-V
HvNAS1   HVPG-IAPARVAFVGSGPLPFSSLVLAAHHLPETQFDNYDLCGAANERARKLFGATADGV
HvNAS5   HVAA---PARVAFIGSGPLPFSSLFLATYHLPDTRFDNYDRCSVANGRAMKLVGAADEGV
          *         *** *********  **  ***  ****    ** **  *  *    *

HvNAS4   GARMSFHTADVADLTDELATYDVVFLAALVGMAAEDKAKVIAHLGAHMADGAALV--ARH
HvNAS7   GARMSFHTADVADLTDELATYDVVFLAALVGMAAEDKGQGDPHLGAHMADGAALVR-SAH
HvNAS6   GARMSFHTADVADLTRELAAYDVVFLAALVGMAAEDKAKVIPHLGAHMADGAALVV-RSA
HvNAS2   GARMSFHTADVADLAGELAKYDVVFLAALVGMAAEDKAKVIAHLGAHMADGAALVVRSAH
HvNAS3   GARMSFHTADVADLASELAKYDVVFLAALVGMAAEDKAKVIAHLGAHMADGAALVVRSAH
HvNAS1   GARMSFHTADVADLTQELGAYDVVFLAALVGMAAEEKAKVIAHLGAHMVEGASLVV-RSA
HvNAS5   RSRMAFHTAEVTDLTAELGAYDVVFLAALVGMTSKEKADAIAHLGKHMADGAVLVREALH
           ** **** * **  **  ************   *   *** **  ** **

HvNAS4   GARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVVNSVIIAQKSNDVHEYGLGSGR--GGR
HvNAS7   GARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVVNSVIIAQKSKDMFANGPRNGC--GGR
HvNAS6   QARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVVNSVIIAHKSKDVHANERPNGR--GGQ
HvNAS2   GARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVVNSVIIAQKSKDVHADGLGSGRGAGGQ
HvNAS3   GARGFLYPIVDPQDIGRGGFEVLAVCHPD-DDVVNSVIIAQKSKEVHADGLGSARGAGRQ
HvNAS1   RPRGFLYPIVDPEDIRRGGFEVLAVHHPE-GEVINSVIVARKAVEAQLSGPQNGD----A
HvNAS5   GARAFLYPVVELDDVGRGGFQVLAVHHPAGDEVFNSFIVARKVKMSA------------
           * **** *   *  **** **** **     * ** * * * *

HvNAS4   YARGTVVPVVSPPCRFG-EMVADVTQ--KREEFANAEVAF
HvNAS7   YARG-TVPVVSPPCRFG-EMVADVTQ--KREEFAKAEVAF
HvNAS6   YRGA--VPVVSPPCRFG-EMVADVTH--KREEFTNAEVAF
HvNAS2   YARG-TVPVVSPPCRFG-EMVADVTQNHKRDEFANAEVAF
HvNAS3   YARG-TVPVVSPPCRFG-EMVADVTQNHKRDEFANAEVAF
HvNAS1   HARG-AVPLVSPPCNFSTKMEASALE--KSEELTAKELAF
            ** ***** *    * *         * *    * **
```

Fig. 8



09/674337

Fig. 9

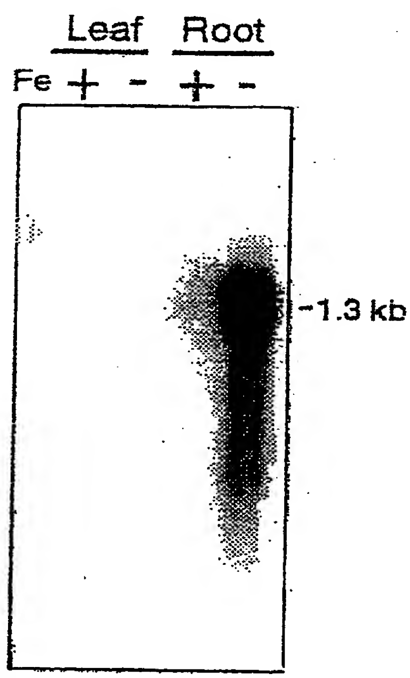


Fig. 10

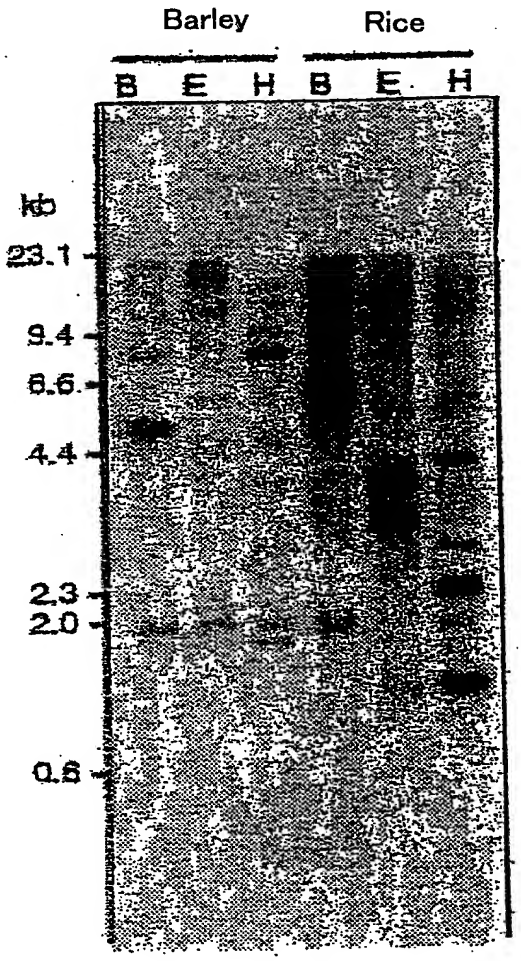


Fig. 11

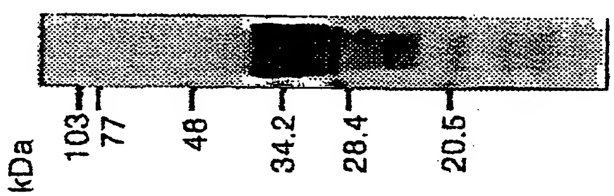


Fig. 12

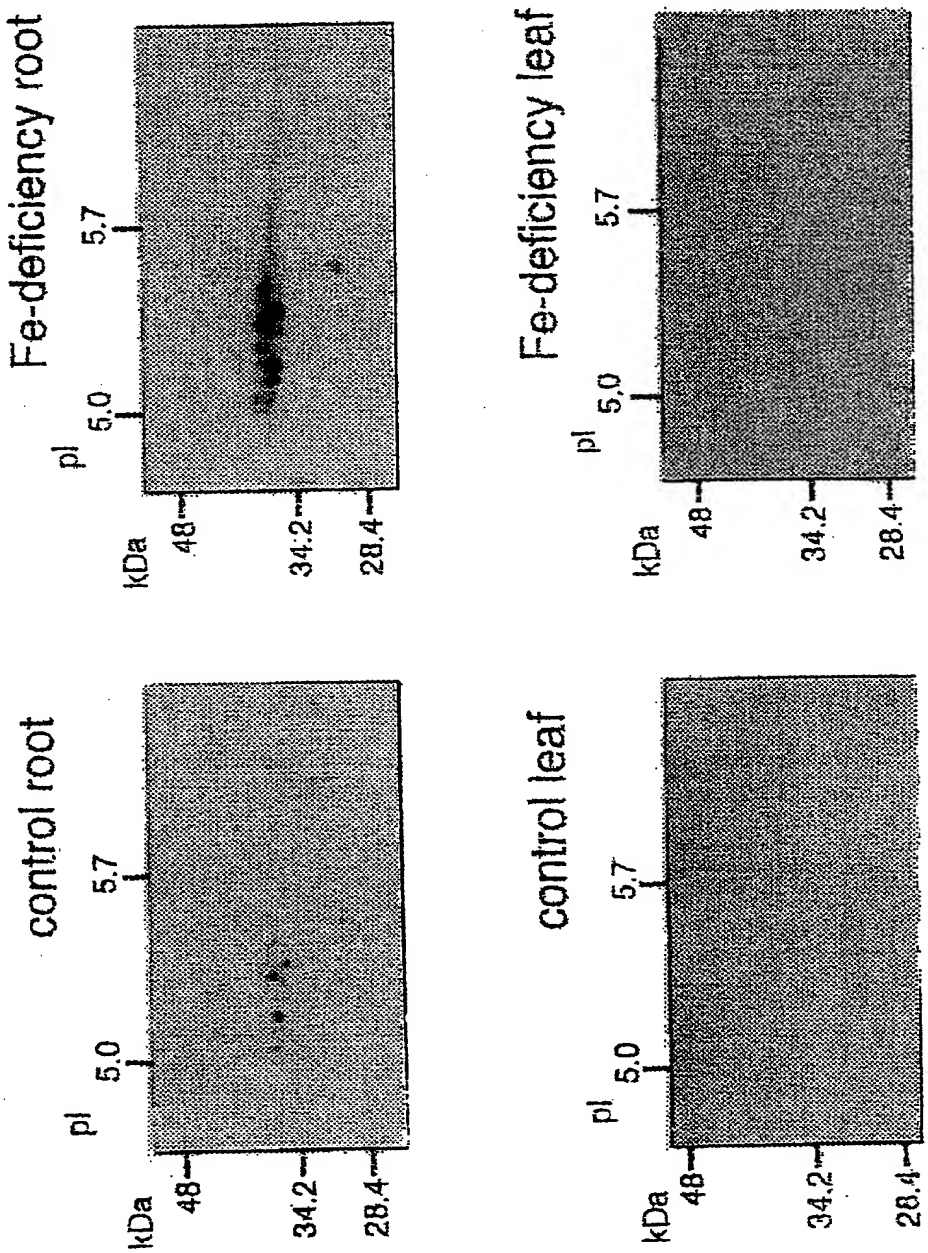
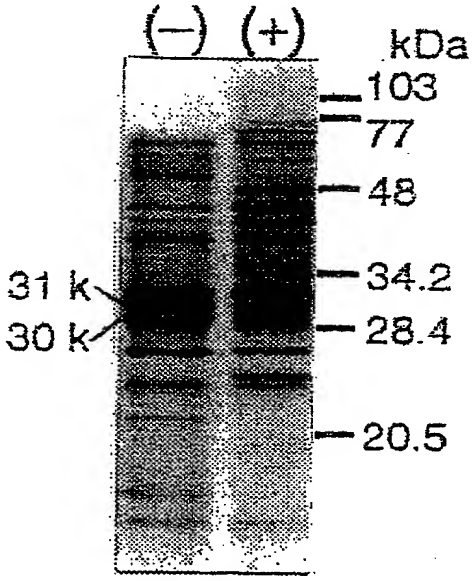


Fig. 13



09/674337

Fig. 14

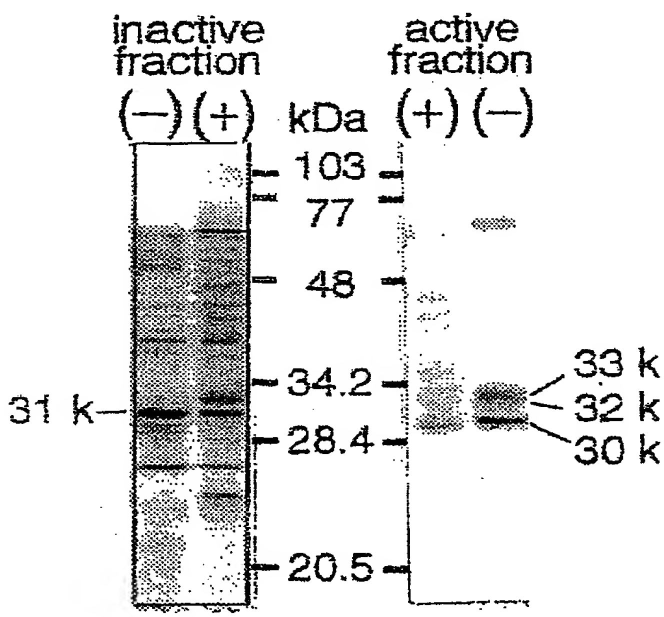


Fig. 15

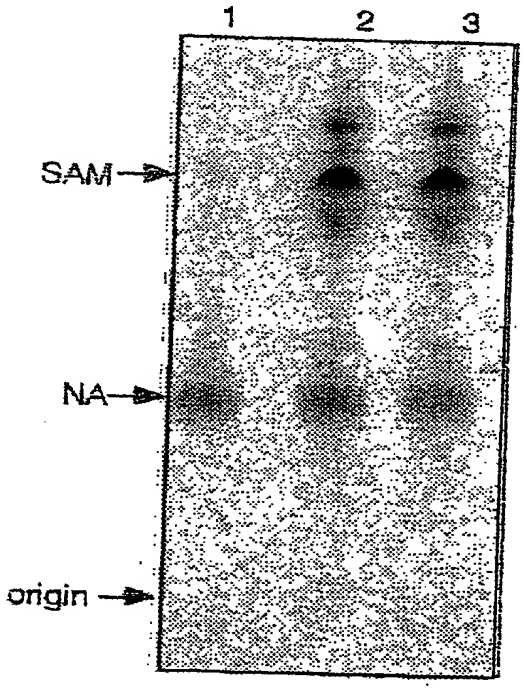


Fig. 16

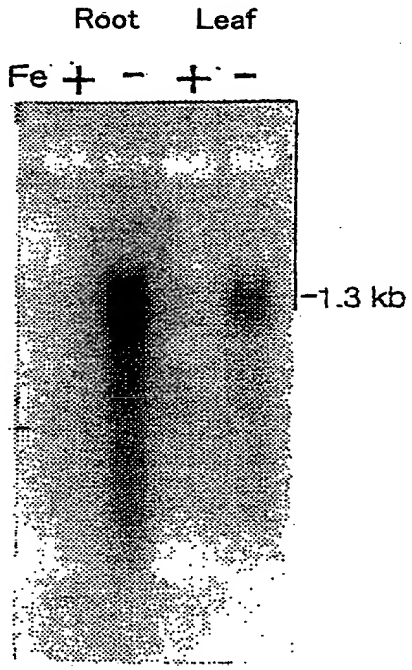


Fig. 17

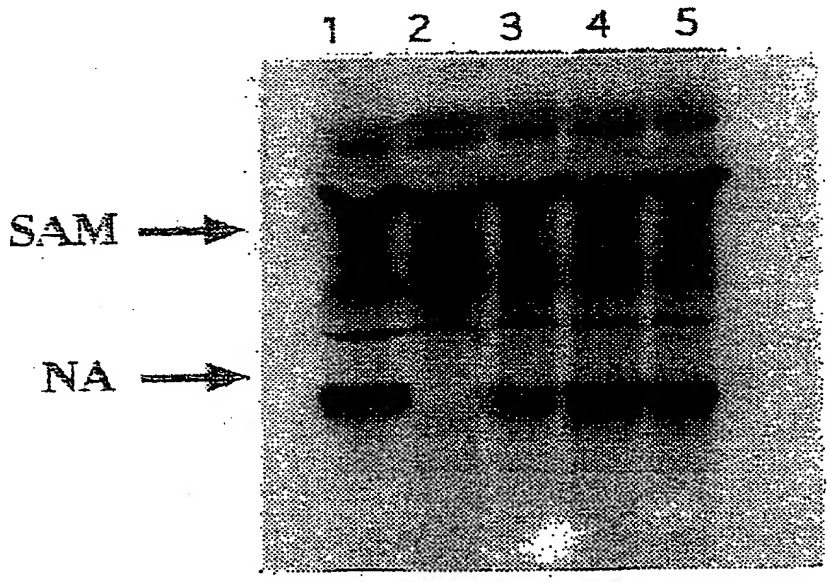


Fig. 18